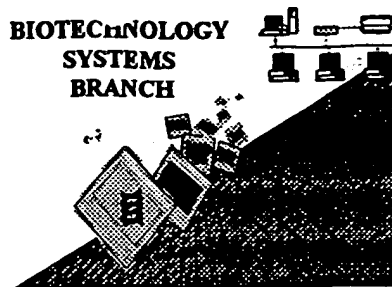


*Dev* *re-run*

**RAW SEQUENCE LISTING**  
**ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/359,426C  
Source: 1645  
Date Processed by STIC: 4/26/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**



# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/359,426C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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AND INTERFERENCE



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1645

MAY 24 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 04/26/2001

PATENT APPLICATION: US/09/359,426C

TIME: 19:15:27

Input Set : N:\Crf3\04202001\I359426B.raw

Output Set: N:\CRF3\04262001\I359426C.raw

Does Not Comply  
Corrected Diskette Needed

1 <110> APPLICANT: Cripps, Alan William  
 2 Clancy, Robert Llewellyn  
 3 Dunkley, Margaret  
 4 <120> TITLE OF INVENTION: Antigen  
 5 <130> FILE REFERENCE: A33655 064727.0105  
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/359,426C  
 7 <141> CURRENT FILING DATE: 1999-07-22  
 8 <150> PRIOR APPLICATION NUMBER: PCT/GB98/00217  
 9 <151> PRIOR FILING DATE: 1998-01-26  
 10 <150> PRIOR APPLICATION NUMBER: GB 9701489.8  
 11 <151> PRIOR FILING DATE: 1997-01-24  
 12 <160> NUMBER OF SEQ ID NOS: 2  
 13 <170> SOFTWARE: FastSEQ for Windows Version 3.0  
 15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 19  
 17 <212> TYPE: PRT  
 18 <213> ORGANISM: P. Aeruginosa  
 19 <220> FEATURE:  
 20 <221> NAME/KEY: DOMAIN  
 21 <222> LOCATION: (1)...(19)  
 22 <223> OTHER INFORMATION: N-terminal sequence  
 23 <221> NAME/KEY: UNSURE  
 24 <222> LOCATION: (1)...(1)  
 25 <223> OTHER INFORMATION: Possibly Ser  
 26 <221> NAME/KEY: UNSURE  
 27 <222> LOCATION: (5)...(6)  
 28 <223> OTHER INFORMATION: Probably Thr-Pro. Possibly Ala-(Lys/Ser)  
 29 <221> NAME/KEY: UNSURE  
 30 <222> LOCATION: (8)...(14)  
 31 <223> OTHER INFORMATION: Probably Thr-Thr-Ala-Ala-Xaa-Ala-Pro. Possibly  
 32 Ala-(Ile/Asp)-Trp-(Phe/Leu)-(Gly/Ser)-Asn-Asp.  
 33 <223> OTHER INFORMATION: Inconclusive sequencing data  
 34 <400> SEQUENCE: 1  
 W--> 35 Xaa Glu Glu Lys Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Val Val  
 36 5 10 15  
 W--> 37 Xaa Asn Ala.  
 39 <210> SEQ ID NO: 2  
 40 <211> LENGTH: 19  
 41 <212> TYPE: PRT  
 42 <213> ORGANISM: P. Aeruginosa  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: DOMAIN  
 45 <222> LOCATION: (1)...(19)  
 46 <223> OTHER INFORMATION: N-terminal sequence  
 47 <221> NAME/KEY: UNSURE  
 48 <222> LOCATION: (1)...(1)  
 49 <223> OTHER INFORMATION: Possibly Ser

pp 1-2

 RECEIVED  
 2001 MAY 23 AM 7:47  
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 AND INTERFERENCES

needs explanation - see item 10 on

Even  
summary  
sheet

If this applies  
 to Xaa at  
 location 17, please  
 insert <221> and  
 response AND  
 <222> 17 above  
 <223> line.

In any case, Xaa at location  
 17 needs explanation. 4/26/01



## RAW SEQUENCE LISTING

DATE: 04/26/2001

PATENT APPLICATION: US/09/359,426C

TIME: 19:15:27

Input Set : N:\Crf3\04202001\I359426B.raw

Output Set: N:\CRF3\04262001\I359426C.raw

50 <221> NAME/KEY: UNSURE  
51 <222> LOCATION: (12)...(12)  
52 <223> OTHER INFORMATION: Possibly Gly or Ser  
53 <223> OTHER INFORMATION: Inconclusive sequencing data  
54 <400> SEQUENCE: 2  
W--> 55 Xaa Glu Glu Lys Thr Pro Leu Thr Thr Ala Ala Xaa Ala Pro Val Val  
56 5 10 15  
W--> 57 Xaa Asn Ala

← same questions (previous  
apply page)  
to this



VERIFICATION SUMMARY

PATENT APPLICATION: US/09/359,426C

DATE: 04/26/2001

TIME: 19:15:28

Input Set : N:\Crf3\04202001\I359426B.raw

Output Set: N:\CRF3\04262001\I359426C.raw

L:6 M:270 C: Current Application Number differs, Wrong Format

L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2

L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2